

SEQUENCE LISTING

<110> Garcia-Martinez, Leon Fernando  
Chen, Yuching  
Andrews, Dawn  
Celltech R&D, Inc.

<120> Modulating Immune Responses

<130> 1427.008US1

<160> 99

<170> FastSEQ for Windows Version 4.0

<210> 1  
<211> 2051  
<212> DNA  
<213> Mus musculus

<400> 1

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<211> 196  
<212> PRT  
<213> Mus musculus

<400> 2

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<210> 3  
<211> 2051  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> A synthetic mutant CD83 sequence

<400> 3

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<210> 4  
<211> 251  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A synthetic mutant CD83 sequence

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Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Leu Ser Tyr Ala
      35          40          45
Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu Ser Val Glu Leu
      50          55          60
Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro Arg Arg Arg Ala
      65          70          75          80
Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser Ser Gly Thr Tyr
      85          90          95
Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn Leu Ser Gly Thr
      100         105         110
Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala Thr Glu Ser Thr
      115         120         125
Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe Ser Leu Val Val
      130         135         140
Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln
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Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu Gln Ala Phe Leu
      165         170         175
Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val Thr Leu Pro Lys
      180         185         190
Thr Glu Thr Val Arg Val Gly Ser Pro Leu Val Phe Thr Lys Pro Arg
      195         200         205
Ala His Gln Ile Ser Val Pro Glu Cys His Pro Asp Lys Arg Arg Met
      210         215         220
Ser Ser Ile Leu Arg Trp Gln Pro Phe Phe Glu Val Leu His Leu Thr
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Val Gly Ser Thr Leu Leu Pro Asp Thr Gly Ser
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<212> DNA
<213> Artificial Sequence
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<220>  
<223> A synthetic mutant CD83 sequence

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<210> 6

<400> 6  
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<210> 7  
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<212> DNA  
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<223> A synthetic mutant CD83 sequence

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<210> 8  
<211> 55  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A synthetic mutant CD83 sequence

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Ser Val Pro Glu Cys His Pro Asp Lys Arg Arg Met Ser Ser Ile Leu  
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Leu Leu Pro Asp Thr Gly Ser  
50 55

<210> 9  
<211> 205  
<212> PRT  
<213> Homo sapiens

<400> 9  
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Trp	Val	Lys	Leu	Leu	Glu	Gly	Gly	Glu	Glu	Arg	Met	Glu	Thr	Pro	Gln
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Glu	Asp	His	Leu	Arg	Gly	Gln	His	Tyr	His	Gln	Lys	Gly	Gln	Asn	Gly
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Ser	Phe	Asp	Ala	Pro	Asn	Glu	Arg	Pro	Tyr	Ser	Leu	Lys	Ile	Arg	Asn
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Asp	Gly	Gln	Arg	Asn	Leu	Ser	Gly	Lys	Val	Ile	Leu	Arg	Val	Thr	Gly
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Cys	Pro	Ala	Gln	Arg	Lys	Glu	Glu	Thr	Phe	Lys	Lys	Tyr	Arg	Ala	Glu
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Ile	Val	Leu	Leu	Leu	Ala	Leu	Val	Ile	Phe	Tyr	Leu	Thr	Leu	Ile	Ile
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Lys	Ala	Gly	Met	Glu	Arg	Ala	Phe	Leu	Pro	Val	Thr	Ser	Pro	Asn	Lys
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<210> 10

<211> 2574

<212> DNA

<213> Homo sapiens

<400> 10

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<210> 11  
<211> 239  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A synthetic 20D04 light chain sequence

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Ser Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ala
      35         40         45
Ser Glu Ser Ile Ser Asn Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly
      50         55         60
Gln Pro Pro Lys Leu Leu Ile Tyr Arg Thr Ser Thr Leu Ala Ser Gly
      65         70         75         80
Val Ser Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Glu Tyr Thr Leu
      85         90         95
Thr Ile Ser Gly Val Gln Cys Asp Asp Val Ala Thr Tyr Tyr Cys Gln
      100        105        110
Cys Thr Ser Gly Gly Lys Phe Ile Ser Asp Gly Ala Ala Phe Gly Gly
      115        120        125
Gly Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu
      130        135        140
Leu Phe Pro Pro Ser Ser Asp Glu Val Ala Thr Gly Thr Val Thr Ile
      145        150        155        160
Val Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu
      165        170        175
Val Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro
      180        185        190
Gln Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu
      195        200        205
Thr Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr
      210        215        220
Gln Gly Thr Thr Ser Val Val Gln Ser Phe Ser Arg Lys Asn Cys
      225        230        235

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<210> 12
<211> 720
<212> DNA
<213> Artificial Sequence
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<220>  
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cagaaccagg	ggcagccctcc	caagctcctg	atctacagga	catccactct	ggcatctggg	240
gtctcatcg	ggttcaaagg	cagtggatct	gggacagagt	acactctcac	catcagcggc	300
gtgcagtgt	acgatgtgc	cacttactac	tgtcaatgca	cttctgggtgg	gaagttcatt	360
atgtatggtg	ctgcttcgg	cgagggacc	gaggtgggtgg	tcaaaggta	tccagttgca	420
cctactgtcc	tcctttccc	accatctac	gatgaggtgg	caactggAAC	agtaccatc	480
gtgtgtgtgg	cgaataaata	ctttcccgat	gtcaccgtca	cctggggaggt	ggatggcacc	540
acccaaacaa	ctggcatcga	gaacagtaaa	acaccgcaga	attctgcaga	ttgtacctac	600
aacctcagca	gcactctgac	actgaccagc	acacagtaca	acagccacaa	agagtacacc	660
tgcaaggtga	cccagggcac	gacctcagtc	gtccagagct	tcagtaggaa	gaactgttaa	720

<210> 13  
<211> 454  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A synthetic 20D04 heavy chain sequence

<400> 13																				
Met	Glu	Thr	Gly	Leu	Arg	Trp	Leu	Leu	Leu	Val	Ala	Val	Leu	Lys	Gly					
1				5				10					15							
Val	Gln	Cys	Gln	Ser	Val	Glu	Glu	Ser	Gly	Gly	Arg	Leu	Val	Thr	Pro					
					20			25				30								
Gly	Thr	Pro	Leu	Thr	Leu	Thr	Cys	Thr	Val	Ser	Gly	Phe	Ser	Leu	Ser					
						35		40			45									
Asn	Asn	Ala	Ile	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu					
						50		55			60									
Trp	Ile	Gly	Tyr	Ile	Trp	Ser	Gly	Gly	Leu	Thr	Tyr	Tyr	Ala	Asn	Trp					
						65		70			75			80						
Ala	Glu	Gly	Arg	Phe	Thr	Ile	Ser	Lys	Thr	Ser	Thr	Thr	Val	Asp	Leu					
						85		90			95									
Lys	Met	Thr	Ser	Pro	Thr	Ile	Glu	Asp	Thr	Ala	Thr	Tyr	Phe	Cys	Ala					
						100		105			110									
Arg	Gly	Ile	Asn	Asn	Ser	Ala	Leu	Trp	Gly	Pro	Gly	Thr	Leu	Val	Thr					
						115		120			125									
Val	Ser	Ser	Gly	Gln	Pro	Lys	Ala	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro					
						130		135			140									
Cys	Cys	Gly	Asp	Thr	Pro	Ser	Ser	Thr	Val	Thr	Leu	Gly	Cys	Leu	Val					
						145		150			155			160						
Lys	Gly	Tyr	Leu	Pro	Glu	Pro	Val	Thr	Val	Thr	Trp	Asn	Ser	Gly	Thr					
						165		170			175									
Leu	Thr	Asn	Gly	Val	Arg	Thr	Phe	Pro	Ser	Val	Arg	Gln	Ser	Ser	Gly					
						180		185			,	190								
Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Ser	Val	Thr	Ser	Ser	Ser	Gln	Pro					
						195		200			205									
Val	Thr	Cys	Asn	Val	Ala	His	Pro	Ala	Thr	Asn	Thr	Lys	Val	Asp	Lys					
						210		215			220									
Thr	Val	Ala	Pro	Ser	Thr	Cys	Ser	Lys	Pro	Thr	Cys	Pro	Pro	Pro	Glu					
						225		230			235			240						
Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp					
						245		250			255									
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp					
						260		265			270									
Val	Ser	Gln	Asp	Asp	Pro	Glu	Val	Gln	Phe	Thr	Trp	Tyr	Ile	Asn	Asn					
						275		280			285									
Glu	Gln	Val	Arg	Thr	Ala	Arg	Pro	Pro	Leu	Arg	Glu	Gln	Gln	Phe	Asn					
						290		295			300									
Ser	Thr	Ile	Arg	Val	Val	Ser	Thr	Leu	Pro	Ile	Ala	His	Gln	Asp	Trp					
						305		310			315			320						
Leu	Arg	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	His	Asn	Lys	Ala	Leu	Pro					
						325		330			335									

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro Leu Glu  
                  340                 345                 350  
 Pro Lys Val Tyr Thr Met Gly Pro Pro Arg Glu Glu Leu Ser Ser Arg  
                  355                 360                 365  
 Ser Val Ser Leu Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser Asp Ile  
                  370                 375                 380  
 Ser Val Glu Trp Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr Lys Thr  
                  385                 390                 395                 400  
 Thr Pro Ala Val Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr Asn Lys  
                  405                 410                 415  
 Leu Ser Val Pro Thr Ser Glu Trp Gln Arg Gly Asp Val Phe Thr Cys  
                  420                 425                 430  
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile  
                  435                 440                 445  
 Ser Arg Ser Pro Gly Lys  
                  450

<210> 14  
 <211> 1362  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A synthetic 20D04 anti-CD83 heavy chain sequence

<400> 14  
 atggagacag gcctgcgctg gcttctcctg gtcgctgtgc tcaaagggtgt ccagtgtcag         60  
 tcggtgagg agtccgggg tcgcctggc acgcctggg caccctgtac actcacctgc         120  
 accgtctctg gattctccct cagaacaat gcaataaaact gggtccggca ggctccaggg         180  
 aaggggctag agtggatcgg atacatttgg agtggtgggc ttacatacta cgcaactgg         240  
 gccgaaggcc gattcaccat ctccaaaacc tcgactacgg tggatctgaa gatgaccagt         300  
 ccgacaatcg aggacacggc cacctatttc tgtgccagag ggattaataa ctccgctttg         360  
 tggggcccaag gcaccctggt caccgtctcc tcagggcaac ctaaggctcc atcagtcttc         420  
 ccactggccc cctgctgcgg ggacacacccc tctagcacgg tgaccttggg ctgcctggc         480  
 aaaggctacc tcccggagcc agtggacttgc accttggact cgggcaccc cacaatggg         540  
 gtacgcacct tcccgtccgt cccgcagttcc tcagccctct actcgctgag cagctgggtg         600  
 agcgtgacct caagcagcca gcccgtcacc tgcaacgtgg cccacccgc cacaacaccc         660  
 aaagtggaca agaccgttgc gcccctcgaca tgcagcaagc ccacgtggcc accccctgaa         720  
 cttctggggg gaccgtctgt cttcatcttc cccccaaaac ccaaggacac cctcatgatc         780  
 tcacgcaccc ccgaggtcac atgcgtgggt gtggacgtga gccaggatga ccccgagggtg         840  
 cagttcacat ggtacataaa caacgagcag gtgcgcaccc cccggccgc gctacggggag         900  
 cagcagttca acagcacgt cccgcgtggc agcaccctcc ccatcgccca ccaggactgg         960  
 ctgaggggca aggagttcaa gtgcaaaagt cacaacaagg cactccggc ccccatcgag         1020  
 aaaaccatct ccaaagccag agggcagccc ctggagccga aggtctacac catggggccct         1080  
 ccccgggagg agctgagcag caggtcggtc agcctgaccc gcatgatcaa cggcttctac         1140  
 ctttcgaca tctcggtgg gtggggagaag aacgggaagg cagaggacaa ctacaagacc         1200  
 acgcccggcc tgctggacag cgacggcttc tacttcctct acaacaagct ctcagtggcc         1260  
 acgagttagt ggcagcgggg cgacgtcttc acctgctccg tcatgcacga ggccttgcac         1320  
 aaccactaca cgcagaagtc catctccgc tctccggta aa                                   1362

<210> 15  
 <211> 238  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A synthetic 11G05 light chain sequence

<400> 15  
 Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Trp  
   1                 5                 10                 15

Leu Pro Gly Ala Arg Cys Ala Asp Val Val Met Thr Gln Thr Pro Ala  
     20                       25                       30  
 Ser Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ser  
     35                       40                       45  
 Ser Lys Asn Val Tyr Asn Asn Trp Leu Ser Trp Phe Gln Gln Lys  
     50                       55                       60  
 Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Thr Leu Ala  
     65                       70                       75                       80  
 Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly Ser Gly Thr Gln Phe  
     85                       90                       95  
 Thr Leu Thr Ile Ser Asp Val Gln Cys Asp Asp Ala Ala Thr Tyr Tyr  
     100                       105                       110  
 Cys Ala Gly Asp Tyr Ser Ser Ser Asp Asn Gly Phe Gly Gly Gly  
     115                       120                       125  
 Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Leu  
     130                       135                       140  
 Phe Pro Pro Ser Ser Asp Glu Val Ala Thr Gly Thr Val Thr Ile Val  
     145                       150                       155                       160  
 Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val  
     165                       170                       175  
 Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln  
     180                       185                       190  
 Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr  
     195                       200                       205  
 Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln  
     210                       215                       220  
 Gly Thr Thr Ser Val Val Gln Ser Phe Ser Arg Lys Asn Cys  
     225                       230                       235

<210> 16

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<223> A synthetic 11G05 anti-CD83 light chain sequence

<400> 16

atggacacca	gggcccccac	ttagctgtcg	gggcctcctgc	tgctctggct	cccgagggcc	60
agatgtgccg	acgtcgatgat	gaccgacact	ccagccctccg	tgtctgcagc	tgtgggaggc	120
acagtccacca	tcaattgcca	gtccagtaag	aatgtttata	ataacaactg	gttacccctgg	180
tttcagcaga	aaccaggggca	gcctcccaag	ctcctgatct	attatgcac	cactctggca	240
tctggggtcc	catcgcgggtt	cagaggcagt	ggatctggga	cacagttcac	tctcaccatt	300
agcgacgtgc	agtgtgacga	tgctgcccact	tactactgtg	caggcgattt	tagtagtagt	360
agtgataatg	gtttccgcgg	agggaccgag	gtgggtgtca	aaggtgatcc	agttgcaccc	420
actgtcctcc	tcttcccacc	atctagcgat	gagggtggcaa	ctggaacagt	caccatcg	480
tgtgtggcga	ataaaatactt	tcccgatgtc	accgtcacct	gggaggtgga	tggcaccacc	540
caaacaactg	gcatcgagaa	cagtaaaaaca	ccgcagaattt	ctgcagattt	tacctacaac	600
ctcagcagca	ctctgacact	gaccagcaca	cagtacaaca	gccacaaaga	gtacacctgc	660
aaggtgaccc	agggcagcag	ctcagtcgtc	cagagcttca	gttaggaagaa	ctgttaa	717

<210> 17

<211> 452

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic 11G05 heavy chain sequence

<400> 17

Met	Glu	Thr	Gly	Leu	Arg	Trp	Leu	Leu	Leu	Val	Ala	Val	Leu	Lys	Gly
1				5				10					15		

Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Thr Pro  
     20                       25                       30  
 Gly Thr Pro Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Thr Ile Ser  
     35                       40                       45  
 Asp Tyr Asp Leu Ser Trp Val Arg Gln Ala Pro Gly Glu Gly Leu Lys  
     50                       55                       60  
 Tyr Ile Gly Phe Ile Ala Ile Asp Gly Asn Pro Tyr Tyr Ala Thr Trp  
     65                       70                       75                       80  
 Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu  
     85                       90                       95  
 Lys Ile Thr Ala Pro Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala  
     100                       105                       110  
 Arg Gly Ala Gly Asp Leu Trp Gly Pro Gly Thr Leu Val Thr Val Ser  
     115                       120                       125  
 Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu Ala Pro Cys Cys  
     130                       135                       140  
 Gly Asp Thr Pro Ser Ser Thr Val Thr Leu Gly Cys Leu Val Lys Gly  
     145                       150                       155                       160  
 Tyr Leu Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Thr Leu Thr  
     165                       170                       175  
 Asn Gly Val Arg Thr Phe Pro Ser Val Arg Gln Ser Ser Gly Leu Tyr  
     180                       185                       190  
 Ser Leu Ser Ser Val Val Ser Val Thr Ser Ser Ser Gln Pro Val Thr  
     195                       200                       205  
 Cys Asn Val Ala His Pro Ala Thr Asn Thr Lys Val Asp Lys Thr Val  
     210                       215                       220  
 Ala Pro Ser Thr Cys Ser Lys Pro Thr Cys Pro Pro Pro Glu Leu Leu  
     225                       230                       235                       240  
 Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu  
     245                       250                       255  
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
     260                       265                       270  
 Gln Asp Asp Pro Glu Val Gln Phe Thr Trp Tyr Ile Asn Asn Glu Gln  
     275                       280                       285  
 Val Arg Thr Ala Arg Pro Pro Leu Arg Glu Gln Gln Phe Asn Ser Thr  
     290                       295                       300  
 Ile Arg Val Val Ser Thr Leu Pro Ile Ala His Gln Asp Trp Leu Arg  
     305                       310                       315                       320  
 Gly Lys Glu Phe Lys Cys Lys Val His Asn Lys Ala Leu Pro Ala Pro  
     325                       330                       335  
 Ile Glu Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro Leu Glu Pro Lys  
     340                       345                       350  
 Val Tyr Thr Met Gly Pro Pro Arg Glu Glu Leu Ser Ser Arg Ser Val  
     355                       360                       365  
 Ser Leu Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser Asp Ile Ser Val  
     370                       375                       380  
 Glu Trp Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr Lys Thr Thr Pro  
     385                       390                       395                       400  
 Ala Val Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr Asn Lys Leu Ser  
     405                       410                       415  
 Val Pro Thr Ser Glu Trp Gln Arg Gly Asp Val Phe Thr Cys Ser Val  
     420                       425                       430  
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile Ser Arg  
     435                       440                       445  
 Ser Pro Gly Lys  
     450

<210> 18  
 <211> 1356  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> A synthetic 11G05 anti-CD83 heavy chain sequence

<400> 18

atggagacag	gcctgcgctg	gcttctcctg	gtcgctgtgc	tcaaagggtgt	ccagtgtcag	60
tcggggagg	agtccgggg	tcgcctggc	acgcctggg	caccctgac	actcacctgc	120
acagtctctg	gattcaccat	cagtgactac	gacttgagct	gggtccggca	ggctccaggg	180
gaggggctga	aatacatcg	attcattgt	attgatggta	accatacta	cgcgacctgg	240
gcaaaaaggcc	gattcaccat	ctccaaaacc	tcgaccacgg	tggatctgaa	aatcaccgct	300
ccgacaaccc	aagacacggc	cacgtatttc	tgtgccagag	gggcagggga	cctctggggc	360
ccagggacc	tcgtcaccgt	ctcttcaggg	caacctaagg	ctccatcagt	cttcccactg	420
gccccctgct	gcggggacac	accctctagc	acggtgacct	tgggctgcct	ggtcaaaggc	480
tacctcccgg	agccagtgc	cgtgacctgg	aactcgggca	ccctcacc	tgggtacgc	540
accttcccgt	ccgtccggca	gtcctcaggg	ctctactcgc	tgagcagcgt	gttgagcgtg	600
acctcaagca	gccagccgt	cacctgcaac	gtggcccacc	cagccaccaa	caccaaagtg	660
gacaagaccg	ttgcgccctc	gacatgcagc	aagcccacgt	gcccacccccc	tgaactcctg	720
gggggaccgt	ctgtcttcat	cttcccccca	aaacccaagg	acaccctcat	gatctcacgc	780
accccccggg	tcacatgcgt	ggtggtggac	gtgagccagg	atgaccccg	gtgtcagttc	840
acatggtaca	taaacaaacga	gcaggtgcgc	accggccggc	cgccgtacg	ggagcagcag	900
ttcaacagca	cgatccgcgt	ggtcagcacc	ctccccatcg	cgcaccagga	ctggctgagg	960
gcaaggagt	tcaagtgc	aa	gtccacaac	aaggcactcc	cgccccccat	1020
atctccaaag	ccagagggca	gcccctggag	ccgaaggct	acaccatggg	ccctccccgg	1080
gaggagctga	gcagcagg	ggtcagcctg	acctgcatga	tcaacggctt	ctacccttcc	1140
gacatctcg	tggagtggga	gaagaacggg	aaggcagagg	acaactacaa	gaccacggc	1200
gccgtctgg	acagcgacgg	ctcctacttc	ctctacaaca	agctctcagt	gcccacgagt	1260
gagtggcagc	ggggcgacgt	cttcacac	tccgtatgc	acgaggcc	gcacaaccac	1320
tacacgcaga	agtccatctc	ccgctctccg	ggtaaa			1356

<210> 19

<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<221> SITE

<222> (1) . . . (238)

<223> Xaa = any amino acid

<220>

<223> A synthetic 14C12 light chain sequence

<400> 19

Met	Asp	Xaa	Arg	Ala	Pro	Thr	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Trp		
1				5				10					15			
Leu	Pro	Gly	Ala	Arg	Cys	Ala	Leu	Val	Met	Thr	Gln	Thr	Pro	Ala	Ser	
							20		25				30			
Val	Ser	Ala	Ala	Ala	Val	Gly	Gly	Thr	Val	Thr	Ile	Asn	Cys	Gln	Ser	Ser
							35		40			45				
Gln	Ser	Val	Tyr	Asp	Asn	Asp	Glu	Leu	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	
							50		55			60				
Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Leu	Ala	Ser	Lys	Leu	Ala	Ser	
							65		70		75		80			
Gly	Val	Pro	Ser	Arg	Phe	Lys	Gly	Ser	Gly	Ser	Gly	Thr	Gln	Phe	Ala	
							85		90			95				
Leu	Thr	Ile	Ser	Gly	Val	Gln	Cys	Asp	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	
							100		105			110				
Gln	Ala	Thr	His	Tyr	Ser	Ser	Asp	Trp	Tyr	Leu	Thr	Phe	Gly	Gly	Gly	
							115		120			125				
Thr	Glu	Val	Val	Val	Lys	Gly	Asp	Pro	Val	Ala	Pro	Thr	Val	Leu	Leu	
							130		135			140				
Phe	Pro	Pro	Ser	Ser	Asp	Glu	Val	Ala	Thr	Gly	Thr	Val	Thr	Ile	Val	
							145		150			155		160		

Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val  
                   165                  170                  175  
 Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln  
                   180                  185                  190  
 Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr  
                   195                  200                  205  
 Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln  
                   210                  215                  220  
 Gly Thr Thr Ser Val Val Gln Ser Phe Ser Arg Lys Asn Cys  
                   225                  230                  235

<210> 20  
 <211> 717  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A synthetic 14C12 anti-CD83 light chain sequence

<400> 20  
 atggacattra gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60  
 agatgtgccctt tttgtatgac ccagactcca gcctccgtgt ctgcagctgt gggaggcaca 120  
 gtcaccatca attgcacagtc cagtcagagt gtttatgata acgacgaatt atcctggtat 180  
 cagcagaaac caggcagcc tcccaagctc ctgatctatc tggcatccaa gttggcatct 240  
 ggggtccccat cccgattcaa aggcaagtga tctggacac agttcgctct caccatcagc 300  
 ggcgtgcagt gtgacgatgc tgccacttac tactgtcaag ccactcatta tagtagtgat 360  
 tggtatctta ctttcggcgg agggaccgag gtgggtgtca aagggtatcc agttgcacct 420  
 actgtcctcc tcttcccacc atctagcgat gaggtggcaa ctggaacagt caccatcgtg 480  
 tggatggcgataataaatactt tcccgatgtc accgtcacct gggaggtgga tggcaccacc 540  
 caaacaaactg gcatcgagaa cagtaaaaaca ccgcagaatt ctgcagattt tacctacaac 600  
 ctcagcagca ctctgacact gaccagcaca cagtacaaca gccacaaaaga gtacacctgc 660  
 aaggtgaccc agggcacgac ctcagtcgtc cagagcttca gtaggaagaa ctgttaa 717

<210> 21  
 <211> 454  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A synthetic 14C12 heavy chain sequence

<400> 21  
 Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly  
     1              5                  10                  15  
 Val His Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Thr Pro  
     20              25                  30  
 Gly Thr Pro Leu Thr Leu Thr Cys Thr Ala Ser Gly Phe Ser Arg Ser  
     35              40                  45  
 Ser Tyr Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu  
     50              55                  60  
 Trp Val Gly Val Ile Ser Thr Ala Tyr Asn Ser His Tyr Ala Ser Trp  
     65              70                  75                  80  
 Ala Lys Gly Arg Phe Thr Ile Ser Arg Thr Ser Thr Thr Val Asp Leu  
     85              90                  95  
 Lys Met Thr Ser Leu Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala  
     100            105                  110  
 Arg Gly Gly Ser Trp Leu Asp Leu Trp Gly Gln Gly Thr Leu Val Thr  
     115            120                  125  
 Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu Ala Pro  
     130            135                  140  
 Cys Cys Gly Asp Thr Pro Ser Ser Thr Val Thr Leu Gly Cys Leu Val  
     145            150                  155                  160

Lys Gly Tyr Leu Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Thr  
                   165                 170                 175  
 Leu Thr Asn Gly Val Arg Thr Phe Pro Ser Val Arg Gln Ser Ser Gly  
                   180                 185                 190  
 Leu Tyr Ser Leu Ser Ser Val Val Ser Val Thr Ser Ser Ser Gln Pro  
                   195                 200                 205  
 Val Thr Cys Asn Val Ala His Pro Ala Thr Asn Thr Lys Val Asp Lys  
                   210                 215                 220  
 Thr Val Ala Pro Ser Thr Cys Ser Lys Pro Thr Cys Pro Pro Pro Glu  
                   225                 230                 235                 240  
 Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp  
                   245                 250                 255  
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
                   260                 265                 270  
 Val Ser Gln Asp Asp Pro Glu Val Gln Phe Thr Trp Tyr Ile Asn Asn  
                   275                 280                 285  
 Glu Gln Val Arg Thr Ala Arg Pro Pro Leu Arg Glu Gln Gln Phe Asn  
                   290                 295                 300  
 Ser Thr Ile Arg Val Val Ser Thr Leu Pro Ile Ala His Gln Asp Trp  
                   305                 310                 315                 320  
 Leu Arg Gly Lys Glu Phe Lys Cys Lys Val His Asn Lys Ala Leu Pro  
                   325                 330                 335  
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro Leu Glu  
                   340                 345                 350  
 Pro Lys Val Tyr Thr Met Gly Pro Pro Arg Glu Glu Leu Ser Ser Arg  
                   355                 360                 365  
 Ser Val Ser Leu Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser Asp Ile  
                   370                 375                 380  
 Ser Val Glu Trp Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr Lys Thr  
                   385                 390                 395                 400  
 Thr Pro Ala Val Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr Asn Lys  
                   405                 410                 415  
 Leu Ser Val Pro Thr Ser Glu Trp Gln Arg Gly Asp Val Phe Thr Cys  
                   420                 425                 430  
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile  
                   435                 440                 445  
 Ser Arg Ser Pro Gly Lys  
                   450

<210> 22  
 <211> 1362  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A synthetic 14C12 anti-CD83 heavy chain sequence

<400> 22  
 Ala Thr Gly Gly Ala Gly Ala Cys Ala Gly Gly Cys Cys Thr Gly Cys  
     1              5                 10                 15  
 Gly Cys Thr Gly Gly Cys Thr Thr Cys Thr Cys Cys Thr Gly Gly Thr  
     20             25                 30  
 Cys Gly Cys Thr Gly Thr Gly Cys Thr Cys Ala Ala Ala Gly Gly Thr  
     35             40                 45  
 Gly Thr Cys Cys Ala Cys Thr Gly Thr Cys Ala Gly Thr Cys Gly Gly  
     50             55                 60  
 Thr Gly Gly Ala Gly Gly Ala Gly Thr Cys Cys Gly Gly Gly Gly  
     65             70                 75                 80  
 Thr Cys Gly Cys Cys Thr Gly Gly Thr Cys Ala Cys Gly Cys Cys Thr  
     85             90                 95  
 Gly Gly Gly Ala Cys Ala Cys Cys Cys Cys Thr Gly Ala Cys Ala Cys  
     100            105                 110

Thr Cys Ala Cys Cys Thr Gly Cys Ala Cys Ala Gly Cys Cys Thr Cys  
 115 120 125  
 Thr Gly Gly Ala Thr Thr Cys Thr Cys Cys Gly Cys Ala Gly Cys  
 130 135 140  
 Ala Gly Cys Thr Ala Cys Gly Ala Cys Ala Thr Gly Ala Gly Cys Thr  
 145 150 155 160  
 Gly Gly Gly Thr Cys Cys Gly Cys Cys Ala Gly Gly Cys Thr Cys Cys  
 165 170 175  
 Ala Gly Gly Ala Ala Gly Gly Cys Thr Gly Gly Ala Ala  
 180 185 190  
 Thr Gly Gly Gly Thr Cys Gly Gly Ala Gly Thr Cys Ala Thr Thr Ala  
 195 200 205  
 Gly Thr Ala Cys Thr Gly Cys Thr Thr Ala Thr Ala Ala Cys Thr Cys  
 210 215 220  
 Ala Cys Ala Cys Thr Ala Cys Gly Cys Gly Ala Gly Cys Thr Gly Gly  
 225 230 235 240  
 Gly Cys Ala Ala Ala Gly Gly Cys Cys Gly Ala Thr Thr Cys Ala  
 245 250 255  
 Cys Cys Ala Thr Cys Thr Cys Ala Gly Ala Ala Cys Cys Thr Cys  
 260 265 270  
 Gly Ala Cys Cys Ala Cys Gly Gly Thr Gly Gly Ala Thr Cys Thr Gly  
 275 280 285  
 Ala Ala Ala Ala Thr Gly Ala Cys Cys Ala Gly Thr Cys Thr Gly Ala  
 290 295 300  
 Cys Ala Ala Cys Cys Gly Ala Ala Gly Ala Cys Ala Cys Gly Gly Cys  
 305 310 315 320  
 Cys Ala Cys Cys Thr Ala Thr Thr Cys Thr Gly Thr Gly Cys Cys  
 325 330 335  
 Ala Gly Ala Gly Gly Gly Thr Ala Gly Thr Thr Gly Gly Thr  
 340 345 350  
 Thr Gly Gly Ala Thr Cys Thr Cys Thr Gly Gly Gly Cys Cys Ala  
 355 360 365  
 Gly Gly Gly Cys Ala Cys Cys Cys Thr Gly Gly Thr Cys Ala Cys Cys  
 370 375 380  
 Gly Thr Cys Thr Cys Cys Thr Cys Ala Gly Gly Cys Ala Ala Cys  
 385 390 395 400  
 Cys Thr Ala Ala Gly Gly Cys Thr Cys Cys Ala Thr Cys Ala Gly Thr  
 405 410 415  
 Cys Thr Thr Cys Cys Ala Cys Thr Gly Gly Cys Cys Cys Cys Cys  
 420 425 430  
 Thr Gly Cys Thr Gly Cys Gly Gly Ala Cys Ala Cys Ala Cys  
 435 440 445  
 Cys Cys Thr Cys Thr Ala Gly Cys Ala Cys Gly Gly Thr Gly Ala Cys  
 450 455 460  
 Cys Thr Thr Gly Gly Cys Thr Gly Cys Cys Thr Gly Gly Thr Cys  
 465 470 475 480  
 Ala Ala Ala Gly Gly Cys Thr Ala Cys Cys Thr Cys Cys Cys Gly Gly  
 485 490 495  
 Ala Gly Cys Cys Ala Gly Thr Gly Ala Cys Cys Gly Thr Gly Ala Cys  
 500 505 510  
 Cys Thr Gly Gly Ala Ala Cys Thr Cys Gly Gly Cys Ala Cys Cys  
 515 520 525  
 Cys Thr Cys Ala Cys Cys Ala Ala Thr Gly Gly Gly Thr Ala Cys  
 530 535 540  
 Gly Cys Ala Cys Cys Thr Thr Cys Cys Gly Thr Cys Cys Gly Thr  
 545 550 555 560  
 Cys Cys Gly Gly Cys Ala Gly Thr Cys Cys Thr Cys Ala Gly Gly Cys  
 565 570 575  
 Cys Thr Cys Thr Ala Cys Thr Cys Gly Cys Thr Gly Ala Gly Cys Ala  
 580 585 590  
 Gly Cys Gly Thr Gly Gly Thr Gly Ala Gly Cys Gly Thr Gly Ala Cys  
 595 600 605

Cys Thr Cys Ala Ala Gly Cys Ala Gly Cys Cys Ala Gly Cys Cys Cys  
 610 615 620  
 Gly Thr Cys Ala Cys Cys Thr Gly Cys Ala Ala Cys Gly Thr Gly Gly  
 625 630 635 640  
 Cys Cys Cys Ala Cys Cys Ala Gly Cys Cys Ala Cys Cys Ala Ala  
 645 650 655  
 Cys Ala Cys Cys Ala Ala Ala Gly Thr Gly Gly Ala Cys Ala Ala Gly  
 660 665 670  
 Ala Cys Cys Gly Thr Thr Gly Cys Cys Cys Cys Thr Cys Gly Ala  
 675 680 685  
 Cys Ala Thr Gly Cys Ala Gly Cys Ala Ala Gly Cys Cys Cys Ala Cys  
 690 695 700  
 Gly Thr Gly Cys Cys Cys Ala Cys Cys Cys Cys Thr Gly Ala Ala  
 705 710 715 720  
 Cys Thr Cys Cys Thr Gly Gly Gly Gly Ala Cys Cys Gly Thr  
 725 730 735  
 Cys Thr Gly Thr Cys Thr Cys Ala Thr Cys Thr Thr Cys Cys Cys  
 740 745 750  
 Cys Cys Cys Ala Ala Ala Ala Cys Cys Cys Ala Ala Gly Gly Ala Cys  
 755 760 765  
 Ala Cys Cys Cys Thr Cys Ala Thr Gly Ala Thr Cys Thr Cys Ala Cys  
 770 775 780  
 Gly Cys Ala Cys Cys Cys Cys Gly Ala Gly Gly Thr Cys Ala Cys  
 785 790 795 800  
 Ala Thr Gly Cys Gly Thr Gly Gly Thr Gly Thr Gly Ala Cys  
 805 810 815  
 Gly Thr Gly Ala Gly Cys Cys Ala Gly Gly Ala Thr Gly Ala Cys Cys  
 820 825 830  
 Cys Cys Gly Ala Gly Gly Thr Gly Cys Ala Gly Thr Thr Cys Ala Cys  
 835 840 845  
 Ala Thr Gly Gly Thr Ala Cys Ala Thr Ala Ala Ala Cys Ala Ala Cys  
 850 855 860  
 Gly Ala Gly Cys Ala Gly Gly Thr Gly Cys Gly Cys Ala Cys Cys Gly  
 865 870 875 880  
 Cys Cys Cys Gly Cys Cys Gly Cys Cys Gly Cys Thr Ala Cys Gly  
 885 890 895  
 Gly Gly Ala Gly Cys Ala Gly Cys Ala Gly Thr Thr Cys Ala Ala Cys  
 900 905 910  
 Ala Gly Cys Ala Cys Gly Ala Thr Cys Cys Gly Cys Gly Thr Gly Gly  
 915 920 925  
 Thr Cys Ala Gly Cys Ala Cys Cys Cys Thr Cys Cys Cys Ala Thr  
 930 935 940  
 Cys Gly Cys Gly Cys Ala Cys Cys Ala Gly Gly Ala Cys Thr Gly Gly  
 945 950 955 960  
 Cys Thr Gly Ala Gly Gly Gly Cys Ala Ala Gly Gly Ala Gly Thr  
 965 970 975  
 Thr Cys Ala Ala Gly Thr Gly Cys Ala Ala Ala Gly Thr Cys Cys Ala  
 980 985 990  
 Cys Ala Ala Cys Ala Ala Gly Gly Cys Ala Cys Thr Cys Cys Cys Gly  
 995 1000 1005  
 Gly Cys Cys Cys Cys Ala Thr Cys Gly Ala Gly Ala Ala Ala Ala  
 1010 1015 1020  
 Cys Cys Ala Thr Cys Thr Cys Cys Ala Ala Ala Gly Cys Cys Ala Gly  
 1025 1030 1035 1040  
 Ala Gly Gly Cys Ala Gly Cys Cys Cys Cys Thr Gly Gly Ala Gly  
 1045 1050 1055  
 Cys Cys Gly Ala Ala Gly Gly Thr Cys Thr Ala Cys Ala Cys Cys Ala  
 1060 1065 1070  
 Thr Gly Gly Cys Cys Cys Thr Cys Cys Cys Gly Gly Gly Ala  
 1075 1080 1085  
 Gly Gly Ala Gly Cys Thr Gly Ala Gly Cys Ala Gly Cys Ala Gly Gly  
 1090 1095 1100

Thr Cys Gly Gly Thr Cys Ala Gly Cys Cys Thr Gly Ala Cys Cys Thr  
 1105 1110 1115 1120  
 Gly Cys Ala Thr Gly Ala Thr Cys Ala Ala Cys Gly Gly Cys Thr Thr  
 1125 1130 1135  
 Cys Thr Ala Cys Cys Thr Thr Cys Cys Gly Ala Cys Ala Thr Cys  
 1140 1145 1150  
 Thr Cys Gly Gly Thr Gly Gly Ala Gly Thr Gly Gly Ala Gly Ala  
 1155 1160 1165  
 Ala Gly Ala Ala Cys Gly Gly Ala Ala Gly Gly Cys Ala Gly Ala  
 1170 1175 1180  
 Gly Gly Ala Cys Ala Ala Cys Thr Ala Cys Ala Ala Gly Ala Cys Cys  
 1185 1190 1195 1200  
 Ala Cys Gly Cys Cys Gly Gly Cys Cys Gly Thr Gly Cys Thr Gly Gly  
 1205 1210 1215  
 Ala Cys Ala Gly Cys Gly Ala Cys Gly Gly Cys Thr Cys Cys Thr Ala  
 1220 1225 1230  
 Cys Thr Thr Cys Cys Thr Cys Thr Ala Cys Ala Ala Cys Ala Ala Gly  
 1235 1240 1245  
 Cys Thr Cys Thr Cys Ala Gly Thr Gly Cys Cys Cys Ala Cys Gly Ala  
 1250 1255 1260  
 Gly Thr Gly Ala Gly Thr Gly Gly Cys Ala Gly Cys Gly Gly Gly  
 1265 1270 1275 1280  
 Cys Gly Ala Cys Gly Thr Cys Thr Thr Cys Ala Cys Cys Thr Gly Cys  
 1285 1290 1295  
 Thr Cys Cys Gly Thr Gly Ala Thr Gly Cys Ala Cys Gly Ala Gly Gly  
 1300 1305 1310  
 Cys Cys Thr Thr Gly Cys Ala Cys Ala Ala Cys Cys Ala Cys Thr Ala  
 1315 1320 1325  
 Cys Ala Cys Gly Cys Ala Gly Ala Ala Gly Thr Cys Cys Ala Thr Cys  
 1330 1335 1340  
 Thr Cys Cys Cys Gly Cys Thr Cys Thr Cys Cys Gly Gly Gly Thr Ala  
 1345 1350 1355 1360  
 Ala Ala

<210> 23  
 <211> 5  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 23  
 Ser Tyr Asp Met Thr  
 1 5

<210> 24  
 <211> 5  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 24  
 Ser Tyr Asp Met Ser  
 1 5

<210> 25  
 <211> 5  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 25  
 Asp Tyr Asp Leu Ser  
 1 5

<210> 26  
<211> 5  
<212> PRT  
<213> Oryctolagus cuniculus

<400> 26  
Ser Tyr Asp Met Ser  
1 5

<210> 27  
<211> 8  
<212> PRT  
<213> Oryctolagus cuniculus

<400> 27  
Tyr Ala Ser Gly Ser Thr Tyr Tyr  
1 5

<210> 28  
<211> 8  
<212> PRT  
<213> Oryctolagus cuniculus

<400> 28  
Ser Ser Ser Gly Thr Thr Tyr Tyr  
1 5

<210> 29  
<211> 8  
<212> PRT  
<213> Oryctolagus cuniculus

<400> 29  
Tyr Ala Ser Gly Ser Thr Tyr Tyr  
1 5

<210> 30  
<211> 8  
<212> PRT  
<213> Oryctolagus cuniculus

<400> 30  
Ala Ile Asp Gly Asn Pro Tyr Tyr  
1 5

<210> 31  
<211> 8  
<212> PRT  
<213> Oryctolagus cuniculus

<400> 31  
Ser Thr Ala Tyr Asn Ser His Tyr  
1 5

<210> 32  
<211> 11  
<212> PRT  
<213> Oryctolagus cuniculus

<400> 32  
Glu His Ala Gly Tyr Ser Gly Asp Thr Gly His  
1 5 10

<210> 33  
<211> 8  
<212> PRT  
<213> Oryctolagus cuniculus

<400> 33  
Glu Gly Ala Gly Val Ser Met Thr  
1 5

<210> 34  
<211> 8  
<212> PRT  
<213> Oryctolagus cuniculus

<400> 34  
Glu Asp Ala Gly Phe Ser Asn Ala  
1 5

<210> 35  
<211> 4  
<212> PRT  
<213> Oryctolagus cuniculus

<400> 35  
Gly Ala Gly Asp  
1

<210> 36  
<211> 6  
<212> PRT  
<213> Oryctolagus cuniculus

<400> 36  
Gly Gly Ser Trp Leu Asp  
1 5

<210> 37  
<211> 5  
<212> PRT  
<213> Oryctolagus cuniculus

<400> 37  
Arg Cys Ala Tyr Asp  
1 5

<210> 38  
<211> 6  
<212> PRT  
<213> Oryctolagus cuniculus

<400> 38  
Arg Cys Ala Asp Val Val  
1 5

<210> 39  
<211> 5  
<212> PRT  
<213> Oryctolagus cuniculus

<400> 39  
Arg Cys Ala Leu Val  
1 5

<210> 40  
<211> 6  
<212> PRT  
<213> Oryctolagus cuniculus

<400> 40  
Gln Ser Ile Ser Thr Tyr  
1 5

<210> 41  
<211> 6  
<212> PRT  
<213> Oryctolagus cuniculus

<400> 41  
Gln Ser Val Ser Ser Tyr  
1 5

<210> 42  
<211> 6  
<212> PRT  
<213> Oryctolagus cuniculus

<400> 42  
Glu Ser Ile Ser Asn Tyr  
1 5

<210> 43  
<211> 8  
<212> PRT  
<213> Oryctolagus cuniculus

<400> 43  
Lys Asn Val Tyr Asn Asn Asn Trp  
1 5

<210> 44  
<211> 12  
<212> PRT  
<213> Oryctolagus cuniculus

<400> 44  
Gln Gln Gly Tyr Thr His Ser Asn Val Asp Asn Val  
1 5 10

<210> 45  
<211> 12  
<212> PRT  
<213> Oryctolagus cuniculus

<400> 45  
 Gln Gln Gly Tyr Ser Ile Ser Asp Ile Asp Asn Ala  
   1               5                   10

<210> 46  
 <211> 14  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 46  
 Gln Cys Thr Ser Gly Gly Lys Phe Ile Ser Asp Gly Ala Ala  
   1               5                   10

<210> 47  
 <211> 11  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 47  
 Ala Gly Asp Tyr Ser Ser Ser Ser Asp Asn Gly  
   1               5                   10

<210> 48  
 <211> 12  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 48  
 Gln Ala Thr His Tyr Ser Ser Asp Trp Leu Thr Tyr  
   1               5                   10

<210> 49  
 <211> 5  
 <212> RNA  
 <213> Oryctolagus cuniculus

<400> 49  
 auuuua   5

<210> 50   6

<211> 6  
 <212> RNA  
 <213> Oryctolagus cuniculus

<400> 50  
 auuuuua   6

<210> 51  
 <211> 7  
 <212> RNA  
 <213> Oryctolagus cuniculus

<400> 51  
 auuuuuua   7

<210> 52  
 <211> 157  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A synthetic anti-CD83 heavy chain variable region sequence

<400> 52  
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly  
1 5 10 15  
Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Thr Pro  
20 25 30  
Gly Thr Pro Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser  
35 40 45  
Ser Tyr Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu  
50 55 60  
Trp Ile Gly Ile Ile Tyr Ala Ser Gly Ser Thr Tyr Tyr Ala Ser Trp  
65 70 75 80  
Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu  
85 90 95  
Glu Val Thr Ser Leu Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ser  
100 105 110  
Arg Glu His Ala Gly Tyr Ser Gly Asp Thr Gly His Leu Trp Gly Pro  
115 120 125  
Gly Thr Leu Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val  
130 135 140  
Phe Pro Leu Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser  
145 150 155

<210> 53  
<211> 154  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A synthetic anti-CD83 heavy chain variable region  
sequence

<400> 53  
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly  
1 5 10 15  
Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Ser Pro  
20 25 30  
Gly Thr Pro Leu Thr Leu Thr Cys Thr Ala Ser Gly Phe Ser Leu Ser  
35 40 45  
Ser Tyr Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu  
50 55 60  
Tyr Ile Gly Ile Ile Ser Ser Ser Gly Thr Thr Tyr Tyr Ala Asn Trp  
65 70 75 80  
Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu  
85 90 95  
Lys Val Thr Ser Pro Thr Ile Gly Asp Thr Ala Thr Tyr Phe Cys Ala  
100 105 110  
Arg Glu Gly Ala Gly Val Ser Met Thr Leu Trp Gly Pro Gly Thr Leu  
115 120 125  
Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu  
130 135 140  
Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser  
145 150

<210> 54  
<211> 154  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A synthetic anti-CD83 heavy chain variable region  
sequence

<400> 54  
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly  
1 5 10 15  
Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Thr Pro  
20 25 30  
Gly Thr Pro Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser  
35 40 45  
Ser Tyr Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu  
50 55 60  
Trp Ile Gly Ile Ile Tyr Ala Ser Gly Ser Thr Tyr Tyr Ala Ser Trp  
65 70 75 80  
Ala Lys Gly Arg Val Ala Ile Ser Lys Thr Ser Thr Thr Val Asp Leu  
85 90 95  
Lys Ile Thr Ser Pro Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala  
100 105 110  
Arg Glu Asp Ala Gly Phe Ser Asn Ala Leu Trp Gly Pro Gly Thr Leu  
115 120 125  
Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu  
130 135 140  
Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser  
145 150

<210> 55

<211> 147

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic anti-CD83 light chain variable region sequence

<400> 55

Met Asp Met Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Trp  
1 5 10 15  
Leu Pro Gly Ala Arg Cys Ala Tyr Asp Met Thr Gln Thr Pro Ala Ser  
20 25 30  
Val Glu Val Ala Val Gly Gly Thr Val Thr Ile Lys Cys Gln Ala Ser  
35 40 45  
Gln Ser Ile Ser Thr Tyr Leu Asp Trp Tyr Gln Gln Lys Pro Gly Gln  
50 55 60  
Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asp Leu Ala Ser Gly Val  
65 70 75 80  
Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Thr Leu Thr  
85 90 95  
Ile Ser Asp Leu Glu Cys Ala Asp Ala Ala Thr Tyr Tyr Cys Gln Gln  
100 105 110  
Gly Tyr Thr His Ser Asn Val Asp Asn Val Phe Gly Gly Thr Glu  
115 120 125  
Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Leu Phe Pro  
130 135 140  
Pro Ser Ser  
145

<210> 56

<211> 147

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic anti-CD83 light chain variable region sequence

<400> 56  
Met Asp Met Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Trp  
1 5 10 15  
Leu Pro Gly Ala Arg Cys Ala Tyr Asp Met Thr Gln Thr Pro Ala Ser  
20 25 30  
Val Glu Val Ala Val Gly Gly Thr Val Ala Ile Lys Cys Gln Ala Ser  
35 40 45  
Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
50 55 60  
Pro Pro Lys Pro Leu Ile Tyr Glu Ala Ser Met Leu Ala Ala Gly Val  
65 70 75 80  
Ser Ser Arg Phe Lys Gly Ser Gly Thr Asp Phe Thr Leu Thr  
85 90 95  
Ile Ser Asp Leu Glu Cys Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gln  
100 105 110  
Gly Tyr Ser Ile Ser Asp Ile Asp Asn Ala Phe Gly Gly Thr Glu  
115 120 125

Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Leu Phe Pro  
130 135 140  
Pro Ser Ser  
145

<210> 57  
<211> 150  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A synthetic anti-CD83 light chain variable region sequence

<400> 57  
Met Asp Met Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Trp  
1 5 10 15  
Leu Pro Gly Ala Arg Cys Ala Asp Val Val Met Thr Gln Thr Pro Ala  
20 25 30  
Ser Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ala  
35 40 45  
Ser Glu Ser Ile Ser Asn Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly  
50 55 60  
Gln Pro Pro Lys Leu Leu Ile Tyr Arg Thr Ser Thr Leu Ala Ser Gly  
65 70 75 80  
Val Ser Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Glu Tyr Thr Leu  
85 90 95  
Thr Ile Ser Gly Val Gln Cys Asp Asp Val Ala Thr Tyr Tyr Cys Gln  
100 105 110  
Cys Thr Ser Gly Gly Lys Phe Ile Ser Asp Gly Ala Ala Phe Gly Gly  
115 120 125  
Gly Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu  
130 135 140  
Leu Phe Pro Pro Ser Ser  
145 150

<210> 58  
<211> 236  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A synthetic M83 020B08L light chain sequence

<400> 58

Met	Asp	Met	Arg	Ala	Pro	Thr	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Trp	
1								5			10			15	
Leu	Pro	Gly	Ala	Arg	Cys	Ala	Tyr	Asp	Met	Thr	Gln	Thr	Pro	Ala	Ser
									20		25			30	
Val	Glu	Val	Ala	Val	Gly	Gly	Thr	Val	Thr	Ile	Lys	Cys	Gln	Ala	Ser
									35		40			45	
Gln	Ser	Ile	Ser	Thr	Tyr	Leu	Asp	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln
									50		55			60	
Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Asp	Ala	Ser	Asp	Leu	Ala	Ser	Gly	Val
65									70		75			80	
Pro	Ser	Arg	Phe	Lys	Gly	Ser	Gly	Ser	Gly	Thr	Gln	Phe	Thr	Leu	Thr
									85		90			95	
Ile	Ser	Asp	Leu	Glu	Cys	Ala	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln
									100		105			110	
Gly	Tyr	Thr	His	Ser	Asn	Val	Asp	Asn	Val	Phe	Gly	Gly	Thr	Glu	
									115		120			125	
Val	Val	Val	Lys	Gly	Asp	Pro	Val	Ala	Pro	Thr	Val	Leu	Leu	Phe	Pro
									130		135			140	
Pro	Ser	Ser	Asp	Glu	Val	Ala	Thr	Gly	Thr	Val	Thr	Ile	Val	Cys	Val
145									150		155			160	
Ala	Asn	Lys	Tyr	Phe	Pro	Asp	Val	Thr	Val	Thr	Trp	Glu	Val	Asp	Gly
									165		170			175	
Thr	Thr	Gln	Thr	Thr	Gly	Ile	Glu	Asn	Ser	Lys	Thr	Pro	Gln	Asn	Ser
									180		185			190	
Ala	Asp	Cys	Thr	Tyr	Asn	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Thr	Ser	Thr
									195		200			205	
Gln	Tyr	Asn	Ser	His	Lys	Glu	Tyr	Thr	Cys	Lys	Val	Thr	Gln	Gly	Thr
									210		215			220	
Thr	Ser	Val	Val	Gln	Ser	Phe	Ser	Arg	Lys	Asn	Cys				
									225		230			235	

<210> 59

<211> 711

<212> DNA

<213> Artificial Sequence

<220>

<223> A synthetic M83 020B08L anti-CD83 light chain sequence

<400> 59

atggacatga	gggcccccac	tcaagtgcgt	gggctcctgc	tgctctggct	cccaagggtgcc	60
agatgtgcct	atgatatgac	ccagactcca	gcctctgtgg	aggttagctgt	gggaggcaca	120
gtcaccatca	agtgcaggc	cagtcagagc	attagtagctt	acttagactg	gtatcagcag	180
aaaccagggc	agcctcccaa	gctcctgtat	tatgtatgtat	ccgatctggc	atctgggtc	240
ccatcgcggt	tcaaaaggcag	tggatctggg	acacagttca	ctctcaccat	cagcgcac	300
gagtgtgcgg	atgctgcac	ttactactgt	caacagggtt	atacacatag	taatgttgat	360
aatgttttcg	gcccggggac	cgagggtgggt	gtcaaagggt	atccagggtc	acctactgtc	420
ctccctttcc	caccatctag	cgatgagggt	gcaactggaa	cagtcaccat	cgtgtgtgt	480
gcaataaaat	actttcccgaa	tgtcacccgtc	acctggggagg	tggatggcac	cacccaaaca	540
actggcatacg	agaacagtaa	aacaccgcag	aattctgcag	attgtaccta	caacctcagc	600
agcactctga	cactgaccag	cacacagtac	aacagccaca	aagagtacac	ctgcaagggt	660
acccaggggca	cgacccatgt	cgtccagagc	ttcagtagga	agaactgtta	a	711

<210> 60

<211> 456

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic M83 020B08H heavy chain sequence

<400> 60  
 Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly  
 1 5 10 15  
 Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Thr Pro  
 20 25 30  
 Gly Thr Pro Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser  
 35 40 45  
 Ser Tyr Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu  
 50 55 60  
 Trp Ile Gly Ile Ile Tyr Ala Ser Gly Thr Thr Tyr Tyr Ala Asn Trp  
 65 70 75 80  
 Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu  
 85 90 95  
 Lys Val Thr Ser Pro Thr Ile Gly Asp Thr Ala Thr Tyr Phe Cys Ala  
 100 105 110  
 Arg Glu Gly Ala Gly Val Ser Met Thr Leu Trp Gly Pro Gly Thr Leu  
 115 120 125  
 Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu  
 130 135 140  
 Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser Thr Val Thr Leu Gly Cys  
 145 150 155 160  
 Leu Val Lys Gly Tyr Leu Pro Glu Pro Val Thr Val Thr Trp Asn Ser  
 165 170 175  
 Gly Thr Leu Thr Asn Gly Val Arg Thr Phe Pro Ser Val Arg Gln Ser  
 180 185 190  
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Ser Val Thr Ser Ser Ser  
 195 200 205  
 Gln Pro Val Thr Cys Asn Val Ala His Pro Ala Thr Asn Thr Lys Val  
 210 215 220  
 Asp Lys Thr Val Ala Pro Ser Thr Cys Ser Lys Pro Thr Cys Pro Pro  
 225 230 235 240  
 Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro  
 245 250 255  
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val  
 260 265 270  
 Val Asp Val Ser Gln Asp Asp Pro Glu Val Gln Phe Thr Trp Tyr Ile  
 275 280 285  
 Asn Asn Glu Gln Val Arg Thr Ala Arg Pro Pro Leu Arg Glu Gln Gln  
 290 295 300  
 Phe Asn Ser Thr Ile Arg Val Val Ser Thr Leu Pro Ile Ala His Gln  
 305 310 315 320  
 Asp Trp Leu Arg Gly Lys Glu Phe Lys Cys Lys Val His Asn Lys Ala  
 325 330 335  
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro  
 340 345 350  
 Leu Glu Pro Lys Val Tyr Thr Met Gly Pro Pro Arg Glu Glu Leu Ser  
 355 360 365  
 Ser Arg Ser Val Ser Leu Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser  
 370 375 380  
 Asp Ile Ser Val Glu Trp Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr  
 385 390 395 400  
 Lys Thr Thr Pro Ala Val Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr  
 405 410 415  
 Asn Lys Leu Ser Val Pro Thr Ser Glu Trp Gln Arg Gly Asp Val Phe  
 420 425 430  
 Thr Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys  
 435 440 445  
 Ser Ile Ser Arg Ser Pro Gly Lys  
 450 455

<210> 61  
 <211> 1368  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A synthetic M83 020B08H anti-CD83 heavy chain sequence

<400> 61

atggagacag	gcctgcgctg	gcttctcccg	gtcgctgtgc	tcaaagggtgt	ccagtgtcag	60
tcgggtggagg	agtccccgggg	tcgcctggc	acgcctggga	caccctgtac	actcacctgc	120
acagtctctg	gattctccct	cagcagctac	gacatgaccc	gggtccggca	ggctccaggg	180
aaggggctgg	aatggatcgg	aatcatttat	gctagtggta	ccacatacta	cgcgaactgg	240
gcgaaaaggcc	gattcaccat	ctccaaaaacc	tcgaccacgg	tggatctgaa	agtcaccagt	300
ccgacaatcg	gggacacggc	cacctatttc	tgtgccagag	agggggctgg	tgttagtatg	360
actttgtggg	gcccaggcac	cctggtcacc	gtctcttcag	ggcaacctaa	ggctccatca	420
gtcttcccac	tggcccccctg	ctgcggggac	acaccctcta	gcacgggtac	cttgggctgc	480
ctggtcaaaag	gtcaccccccc	ggagccagtg	acgtgaccc	ggaactctggg	caccctcacc	540
aatgggggtac	gcacccccc	gtccgtccgg	cagtcctcag	gcctctactc	gctgagcagc	600
gtggtgagcg	tgacctaag	cagccagccc	gtcacctgca	acgtggccca	cccagccacc	660
aacacccaaag	tggacaagac	cgttgcgc	tcgacatgca	gcaagccac	gtgcccaccc	720
cctgaactcc	tggggggacc	gtctgtcttc	atctccccc	caaaccacaa	ggacaccctc	780
atgatctcac	gcaccccccga	gttcacatgc	gtgggtgtgg	acgtgagcca	ggatgacccc	840
gaggtgcagt	tcacatggta	cataaaacaac	gagcaggtgc	gcaccggcc	gccgccccta	900
cgggagcagc	agttcaaacag	cacgatccgc	gtggtcagca	ccctcccat	cgcgcaccag	960
gactggctga	ggggcaagga	gttcaagtg	aaagtccaca	acaaggcact	cccgcccccc	1020
atcgagaaaa	ccatctccaa	agccagaggg	cagccctgg	agccgaaggt	ctacaccatg	1080
ggccctcccc	gggaggagct	gagcagcagg	tcggtagcc	tgacctgcac	gatcaacggc	1140
ttctaccctt	ccgacatctc	ggtggagttg	gagaagaacg	ggaaggcaga	ggacaactac	1200
aagaccacgc	cggccgtgt	ggacagcgc	ggctctact	tcctctacaa	caagctctca	1260
gtgcccacga	gtgagtgcc	gccccggcgc	gtcttcaccc	gctccgtgt	gcacgaggcc	1320
ttgcacaacc	actacacgc	gaagtccatc	tcccgctctc	cgggtaaa		1368

<210> 62  
 <211> 236  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A synthetic M83 006G05L light chain sequence

<400> 62

Met	Asp	Met	Arg	Ala	Pro	Thr	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Trp		
1								5			10			15		
Leu	Pro	Gly	Ala	Arg	Cys	Ala	Tyr	Asp	Met	Thr	Gln	Thr	Pro	Ala	Ser	
									20		25			30		
Val	Glu	Val	Ala	Val	Gly	Gly	Thr	Val	Ala	Ile	Lys	Cys	Gln	Ala	Ser	
									35		40			45		
Gln	Ser	Val	Ser	Ser	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	
									50		55			60		
Pro	Pro	Lys	Pro	Leu	Ile	Tyr	Glu	Ala	Ser	Met	Leu	Ala	Ala	Gly	Val	
									65		70			75		80
Ser	Ser	Arg	Phe	Lys	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	
									85		90			95		
Ile	Ser	Asp	Leu	Glu	Cys	Asp	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	
									100		105			110		
Gly	Tyr	Ser	Ile	Ser	Asp	Ile	Asp	Asn	Ala	Phe	Gly	Gly	Gly	Thr	Glu	
									115		120			125		
Val	Val	Val	Lys	Gly	Asp	Pro	Val	Ala	Pro	Thr	Val	Leu	Leu	Phe	Pro	
									130		135			140		

Pro Ser Ser Asp Glu Val Ala Thr Gly Thr Val Thr Ile Val Cys Val  
 145 150 155 160  
 Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val Asp Gly  
 165 170 175  
 Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln Asn Ser  
 180 185 190  
 Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr Ser Thr  
 195 200 205  
 Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln Gly Thr  
 210 215 220  
 Thr Ser Val Val Gln Ser Phe Ser Arg Lys Asn Cys  
 225 230 235

<210> 63  
 <211> 711  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A synthetic M83 006G05L anti-CD83 light chain sequence

<400> 63  
 atggacatga gggcccccac tcaactgctg gggctcctgc tgctctggct cccaggtgcc 60  
 agatgtgcct atgatatgac ccagactcca gcctctgtgg aggttagctgt gggaggcaca 120  
 gtcgccatca agtgccaggc cagtcagagc gtttagtagtt acttagcctg gtatcagcag 180  
 aaaccagggc agcctccaa gcccctgatc tacgaagcat ccatgctggc ggctggggtc 240  
 tcatcgcggt tcaaaggcag tggatctggg acagacttca ctctcaccat cagcgacctg 300  
 gagtgtgacg atgctgccac ttactattgt caacagggtt attctatcag tggatattgt 360  
 aatgcttcg gcgaggggac cgaggtggg gtcaaaagggtt atccagttgc acctactgtc 420  
 ctcctttcc caccatctag cgatgaggtt gcaactggaa cagtaccat cgtgtgttg 480  
 gcaataaaat actttccga tgcaccgtc acctggggagg tggatggcac cacccaaaca 540  
 actggcatcg agaacagtaa aacaccgcag aattctgcag attgtaccta caacctcagc 600  
 agactctga cactgaccag cacacagttac aacagccaca aagagtacac ctgcaagggtg 660  
 acccaggcga cgacccatcg cgtccagagc ttccatggaa agaactgtta a 711

<210> 64  
 <211> 459  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A synthetic M83 006G05L heavy chain sequence

<400> 64  
 Met Glu Thr Gly Leu Arg Trp Leu Leu Val Ala Val Leu Lys Gly  
 1 5 10 15  
 Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Ser Pro  
 20 25 30  
 Gly Thr Pro Leu Thr Leu Thr Cys Thr Ala Ser Gly Phe Ser Leu Ser  
 35 40 45  
 Ser Tyr Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu  
 50 55 60  
 Tyr Ile Gly Ile Ile Ser Ser Ser Gly Ser Thr Tyr Tyr Ala Ser Trp  
 65 70 75 80  
 Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu  
 85 90 95  
 Glu Val Thr Ser Leu Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ser  
 100 105 110  
 Arg Glu His Ala Gly Tyr Ser Gly Asp Thr Gly His Leu Trp Gly Pro  
 115 120 125

Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gln	Pro	Lys	Ala	Pro	Ser	Val
130					135					140					
Phe	Pro	Leu	Ala	Pro	Cys	Cys	Gly	Asp	Thr	Pro	Ser	Ser	Thr	Val	Thr
145					150				155						160
Leu	Gly	Cys	Leu	Val	Lys	Gly	Tyr	Leu	Pro	Glu	Pro	Val	Thr	Val	Thr
					165				170						175
Trp	Asn	Ser	Gly	Thr	Leu	Thr	Asn	Gly	Val	Arg	Thr	Phe	Pro	Ser	Val
					180				185						190
Arg	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Ser	Val	Thr
					195				200						205
Ser	Ser	Gln	Pro	Val	Thr	Cys	Asn	Val	Ala	His	Pro	Ala	Thr	Asn	
					210				215						220
Thr	Lys	Val	Asp	Lys	Thr	Val	Ala	Pro	Ser	Thr	Cys	Ser	Lys	Pro	Thr
					225				230						240
Cys	Pro	Pro	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro
					245				250						255
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr
					260				265						270
Cys	Val	Val	Val	Asp	Val	Ser	Gln	Asp	Asp	Pro	Glu	Val	Gln	Phe	Thr
					275				280						285
Trp	Tyr	Ile	Asn	Asn	Glu	Gln	Val	Arg	Thr	Ala	Arg	Pro	Pro	Leu	Arg
					290				295						300
Glu	Gln	Gln	Phe	Asn	Ser	Thr	Ile	Arg	Val	Val	Ser	Thr	Leu	Pro	Ile
					305				310						320
Ala	His	Gln	Asp	Trp	Leu	Arg	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	His
					325				330						335
Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Arg
					340				345						350
Gly	Gln	Pro	Leu	Glu	Pro	Lys	Val	Tyr	Thr	Met	Gly	Pro	Pro	Arg	Glu
					355				360						365
Glu	Leu	Ser	Ser	Arg	Ser	Val	Ser	Leu	Thr	Cys	Met	Ile	Asn	Gly	Phe
					370				375						380
Tyr	Pro	Ser	Asp	Ile	Ser	Val	Glu	Trp	Glu	Lys	Asn	Gly	Lys	Ala	Glu
					385				390						400
Asp	Asn	Tyr	Lys	Thr	Thr	Pro	Ala	Val	Leu	Asp	Ser	Asp	Gly	Ser	Tyr
					405				410						415
Phe	Leu	Tyr	Asn	Lys	Leu	Ser	Val	Pro	Thr	Ser	Glu	Trp	Gln	Arg	Gly
					420				425						430
Asp	Val	Phe	Thr	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
					435				440						445
Thr	Gln	Lys	Ser	Ile	Ser	Arg	Ser	Pro	Gly	Lys					
					450				455						

<210> 65  
<211> 1377  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> A synthetic M83 006G05L anti-CD83 heavy chain sequence

<400> 65  
atggagacag gcctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag 60  
tcggtgagg agtccgggg tcgcctggc tcgcctggg caccctgac actcacctgc 120  
acagcctctg gattccccc cagtagctac gacatgagct gggtccgcca ggctccaggg 180  
aaggggctgg aatacatcggt aatcattttt agtagtggtt gcacatacta cgcgagctgg 240  
gcaaaaggcc gattcaccat ctccaaaacc tcgaccacgg tggatctggg agtgaccagt 300  
ctgacaaccg aggacacggc cacctatttc tgttagtagag aacatgctgg ttatagtgg 360  
gatacgggtc acttgtgggg cccaggcacc ctggtcaccg tctcctcgaa gcaacctaag 420

gctccatcg tcttcccact	ggccccctgc	tgcggggaca	caccctctag	cacggtgacc	480
ttgggctgcc	tggtaaaagg	ctacctcccg	gagccagtga	ccgtgacctg	540
accctcacca	atgggtacg	cacccccc	tccgtccggc	agtcctcagg	600
ctgagcagcg	tggtgagcgt	gacctaagc	agccagcccg	tcacctgaa	660
ccagccacca	acaccaaagt	ggacaagacc	gttgcgcct	cgacatgcag	720
tgcccacccc	ctgaactcct	ggggggaccc	tctgtctca	tcttcccccc	780
gacacccctca	tgatctcagc	cacccccc	gtcacatgcg	tggtggtgga	840
gatgaccccg	aggtcagtt	cacatggta	ataaacaacg	agcaggtgcg	900
ccgcgcgtac	gggagcagca	gttcaacacg	acgatcccg	tggtcagcac	960
gcmcaccagg	actggctgag	gggcaaggag	ttcaagtgc	aagtccacaa	1020
ccggccccca	tcgagaaaac	catctccaaa	gccagaggc	caaggcactc	1080
tacaccatgg	gccctcccc	ggaggagctg	agcagcagg	cggtcagcct	1140
atcaacggct	tctacccttc	cgacatctcg	gtggagtggg	agaagaacgg	1200
gacaactaca	agaccacg	gcgcgtctg	gacagcga	gctcctactc	1260
aagctctcag	tgcccacgag	tgagtggcag	cggggcgacg	tcttcacctg	1320
cacgaggcct	tgcacaacca	ctacacgcag	aagtccatct	ctccgtgtatg	1377

<210> 66

<211> 150

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic anti-CD83 heavy chain variable region sequence

<400> 66

Met	Glu	Thr	Gly	Leu	Arg	Trp	Leu	Leu	Leu	Val	Ala	Val	Leu	Lys	Gly
1				5				10					15		
Val	Gln	Cys	Gln	Ser	Val	Glu	Glu	Ser	Gly	Gly	Arg	Leu	Val	Thr	Pro
								20				25		30	
Gly	Thr	Pro	Leu	Thr	Leu	Thr	Cys	Thr	Val	Ser	Gly	Phe	Thr	Ile	Ser
								35			40		45		
Asp	Tyr	Asp	Leu	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Glu	Gly	Leu	Lys
								50		55		60			
Tyr	Ile	Gly	Phe	Ile	Ala	Ile	Asp	Gly	Asn	Pro	Tyr	Tyr	Ala	Thr	Trp
								65		70		75		80	
Ala	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Lys	Thr	Ser	Thr	Thr	Val	Asp	Leu
								85		90		95			
Lys	Ile	Thr	Ala	Pro	Thr	Thr	Glu	Asp	Thr	Ala	Thr	Tyr	Phe	Cys	Ala
								100		105		110			
Arg	Gly	Ala	Gly	Asp	Leu	Trp	Gly	Pro	Gly	Thr	Leu	Val	Thr	Val	Ser
								115		120		125			
Ser	Gly	Gln	Pro	Lys	Ala	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Cys
								130		135		140			
Gly	Asp	Thr	Pro	Ser	Ser										
								145		150					

<210> 67

<211> 152

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic anti-CD83 heavy chain variable region sequence

<400> 67

Met	Glu	Thr	Gly	Leu	Arg	Trp	Leu	Leu	Leu	Val	Ala	Val	Leu	Lys	Gly
1				5				10					15		
Val	His	Cys	Gln	Ser	Val	Glu	Glu	Ser	Gly	Gly	Arg	Leu	Val	Thr	Pro
								20		25		30			

Gly Thr Pro Leu Thr Leu Thr Cys Thr Ala Ser Gly Phe Ser Arg Ser  
     35                        40                        45  
 Ser Tyr Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu  
     50                        55                        60  
 Trp Val Gly Val Ile Ser Thr Ala Tyr Asn Ser His Tyr Ala Ser Trp  
     65                        70                        75                        80  
 Ala Lys Gly Arg Phe Thr Ile Ser Arg Thr Ser Thr Thr Val Asp Leu  
     85                        90                        95  
 Lys Met Thr Ser Leu Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala  
     100                       105                       110  
 Arg Gly Gly Ser Trp Leu Asp Leu Trp Gly Gln Gly Thr Leu Val Thr  
     115                       120                       125  
 Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu Ala Pro  
     130                       135                       140  
 Cys Cys Gly Asp Thr Pro Ser Ser  
     145                       150

<210> 68  
 <211> 149  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A synthetic anti-CD83 light chain variable region  
 sequence

<400> 68  
 Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Trp  
   1                       5                           10                       15  
 Leu Pro Gly Ala Arg Cys Ala Asp Val Val Met Thr Gln Thr Pro Ala  
   20                       25                           30  
 Ser Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ser  
   35                       40                           45  
 Ser Lys Asn Val Tyr Asn Asn Asn Trp Leu Ser Trp Phe Gln Gln Lys  
   50                       55                           60  
 Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Thr Leu Ala  
   65                       70                           75                       80  
 Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly Ser Gly Thr Gln Phe  
   85                       90                           95  
 Thr Leu Thr Ile Ser Asp Val Gln Cys Asp Asp Ala Ala Thr Tyr Tyr  
   100                      105                           110  
 Cys Ala Gly Asp Tyr Ser Ser Ser Asp Asn Gly Phe Gly Gly Gly  
   115                      120                           125  
 Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Leu  
   130                      135                           140  
 Phe Pro Pro Ser Ser  
   145

<210> 69  
 <211> 149  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <221> SITE  
 <222> (1)...(149)  
 <223> Xaa = any amino acid

<220>  
 <223> A synthetic anti-CD83 light chain variable region  
 sequence

<400> 69  
Met Asp Xaa Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Trp  
1 5 10 15  
Leu Pro Gly Ala Arg Cys Ala Leu Val Met Thr Gln Thr Pro Ala Ser  
20 25 30  
Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ser Ser  
35 40 45  
Gln Ser Val Tyr Asp Asn Asp Glu Leu Ser Trp Tyr Gln Gln Lys Pro  
50 55 60  
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser Lys Leu Ala Ser  
65 70 75 80  
Gly Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Ala  
85 90 95  
Leu Thr Ile Ser Gly Val Gln Cys Asp Asp Ala Ala Thr Tyr Tyr Cys  
100 105 110  
Gln Ala Thr His Tyr Ser Ser Asp Trp Tyr Leu Thr Phe Gly Gly Gly  
115 120 125  
Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Leu  
130 135 140  
Phe Pro Pro Ser Ser  
145

<210> 70  
<211> 240  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A synthetic 96G08 light chain sequence

<400> 70  
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Trp  
1 5 10 15  
Leu Pro Gly Ala Thr Phe Ala Gln Val Leu Thr Gln Thr Ala Ser Pro  
20 25 30  
Val Ser Ala Pro Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ser Ser  
35 40 45  
Gln Ser Val Tyr Asn Asn Asp Phe Leu Ser Trp Tyr Gln Gln Lys Pro  
50 55 60  
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Thr Leu Ala Ser  
65 70 75 80  
Gly Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Thr  
85 90 95  
Leu Thr Ile Ser Asp Leu Glu Cys Asp Asp Ala Ala Thr Tyr Tyr Cys  
100 105 110  
Thr Gly Thr Tyr Gly Asn Ser Ala Trp Tyr Glu Asp Ala Phe Gly Gly  
115 120 125  
Gly Thr Glu Val Val Val Lys Arg Thr Pro Val Ala Pro Thr Val Leu  
130 135 140  
Leu Phe Pro Pro Ser Ser Ala Glu Leu Ala Thr Gly Thr Ala Thr Ile  
145 150 155 160  
Val Cys Val Ala Asn Lys Tyr Phe Pro Asp Gly Thr Val Thr Trp Lys  
165 170 175  
Val Asp Gly Ile Thr Gln Ser Ser Gly Ile Asn Asn Ser Arg Thr Pro  
180 185 190  
Gln Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu  
195 200 205  
Ser Ser Asp Glu Tyr Asn Ser His Asp Glu Tyr Thr Cys Gln Val Ala  
210 215 220  
Gln Asp Ser Gly Ser Pro Val Val Gln Ser Phe Ser Arg Lys Ser Cys  
225 230 235 240

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<210> 71
<211> 13
<212> PRT
<213> Oryctolagus cuniculus

<400> 71
Gln Ser Ser Gln Ser Val Tyr Asn Asn Asp Phe Leu Ser
1 5 10

<210> 72
<211> 7
<212> PRT
<213> Oryctolagus cuniculus

<400> 72
Tyr Ala Ser Thr Leu Ala Ser
1 5

<210> 73
<211> 13
<212> PRT
<213> Oryctolagus cuniculus

<400> 73
Thr Gly Thr Tyr Gly Asn Ser Ala Trp Tyr Glu Asp Ala
1 5 10

<210> 74
<211> 723
<212> DNA
<213> Artificial Sequence

<220>
<223> A synthetic 96G08 anti-CD83 light chain sequence

<400> 74
atggacacga gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60
acatttgcgc aagtgcgtac ccagactgca tcgcccgtgt ctgcacctgt gggaggcaca 120
gtcaccatca attgccagtc cagtcagagt gtttataata acgacttctt atcctggtat 180
cagcagaaac cagggcagcc tcccaaactc ctgatctatt atgcatccac tctggcatct 240
gggtccccat ccccggttcaa aggcaagtggc tctggacac agttcaactt caccatcagc 300
gacctggagt gtgacgatgc tgccacttac tactgtacag gcacttatgg taatagtgtct 360
tggtacgagg atgccttcgg cggagggacc gaggtgggtgg tcaaacgtac gccagttgca 420
cctactgtcc tcctcttccc accatcttagc gctgagctgg caactggAAC agccaccatc 480
gtgtgcgtgg cgaataaaata ctttcccgat ggcacccgtca cctggaaaggt ggatggcatc 540
acccaaagca gcggcatcaa taacagtaga acaccgcaga attctgcaga ttgtacctac 600
aacctcagca gtactctgac actgagcagc gacgagtaca acagccacga cgagtacacc 660
tgccaggtgg cccaggactc aggctcaccc gtcgtccaga gtttcagtag gaagagctgt 720
tag 723

<210> 75
<211> 25
<212> DNA
<213> Oryctolagus cuniculus

<400> 75
cagtccagtc agagtgttta taata 25

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<210> 76		
<211> 20		
<212> DNA		
<213> Oryctolagus cuniculus		
<400> 76		
atgcatccac tctggcatct		20
<210> 77		
<211> 25		
<212> DNA		
<213> Oryctolagus cuniculus		
<400> 77		
acaggcactt atggtaatag tgctt		25
<210> 78		
<211> 456		
<212> PRT		
<213> Artificial Sequence		
<220>		
<223> A synthetic 96G08 heavy chain sequence		
<400> 78		
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly		
1 5 10 15		
Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Thr Pro		
20 25 30		
Gly Thr Pro Leu Thr Leu Thr Cys Thr Val Ser Gly Ile Asp Leu Ser		
35 40 45		
Ser Asp Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu		
50 55 60		
Trp Ile Gly Ile Ile Ser Ser Gly Gly Asn Thr Tyr Tyr Ala Ser Trp		
65 70 75 80		
Ala Lys Gly Arg Phe Thr Ile Ser Arg Thr Ser Thr Thr Val Asp Leu		
85 90 95		
Lys Met Thr Ser Leu Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala		
100 105 110		
Arg Val Val Gly Gly Thr Tyr Ser Ile Trp Gly Gln Gly Thr Leu Val		
115 120 125		
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Tyr Pro Leu Ala		
130 135 140		
Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu		
145 150 155 160		
Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly		
165 170 175		
Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp		
180 185 190		
Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro		
195 200 205		
Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys		
210 215 220		
Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile		
225 230 235 240		
Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro		
245 250 255		
Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val		
260 265 270		
Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val		
275 280 285		

Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln  
 290 295 300  
 Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln  
 305 310 315 320  
 Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala  
 325 330 335  
 Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro  
 340 345 350  
 Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala  
 355 360 365  
 Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu  
 370 375 380  
 Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr  
 385 390 395 400  
 Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr  
 405 410 415  
 Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe  
 420 425 430  
 Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His Thr Glu Lys  
 435 440 445  
 Ser Leu Ser His Ser Pro Gly Lys  
 450 455

<210> 79  
 <211> 5  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 79  
 Ser Asp Gly Ile Ser  
 1 5

<210> 80  
 <211> 16  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 80  
 Ile Ile Ser Ser Gly Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys Gly  
 1 5 10 15

<210> 81  
 <211> 8  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 81  
 Val Val Gly Gly Thr Tyr Ser Ile  
 1 5

<210> 82  
 <211> 1371  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A synthetic 96G08 anti-CD83 heavy chain sequence

<400> 82  
 atggagactg ggctgcgctg gtttcctcg gtcgtgtgc tcaaagggtgt ccagtgtcag 60  
 tcggtgagg agtccggggg tcgcctggtc acacctggga caccctgac actcacctgc 120

acagtgtctg	aatcgacct	cagtagcgat	ggaataagct	gggtccggca	ggctccaggg	180
aaggggctgg	aatggatcg	aatcattagt	agtgtggta	acacatacta	cgcgagctgg	240
gcaaaaaggc	gattcacat	ctccagaacc	tcgaccacgg	tggatctgaa	gatgaccagt	300
ctgacaaccg	aggacacggc	cacctattc	tgtgccagag	ttgttggtg	tacttatagc	360
atctggggcc	agggcaccct	cgtcaccgtc	tcgagcgctt	ctacaaaagg	cccatctgtc	420
tatccactgg	cccctggatc	tgctgccccaa	actaactcca	tggtgaccct	ggatgcctg	480
gtcaaggggct	atttcctga	gccagtgaca	gtgacctgga	actctggatc	cctgtccagc	540
ggtgtgcaca	ccttcccagc	tgtcctgcag	tctgacctt	acactctgag	cagtcagtg	600
actgtcccct	ccagcacctg	gcccagcgag	accgtcacct	gcaacgtgc	ccacccggcc	660
agcagcacca	aggtggacaa	aaaaattgtg	cccagggatt	gtggttgtaa	gccttgcata	720
tgtagcgtcc	cagaagtata	atctgtctc	atctcccccc	caaagccaa	ggatgtgtc	780
accattactc	tgactctaa	gtcacgtt	gttgggttag	acatcagaa	ggatgatccc	840
gaggtccagt	ttagctggtt	ttagatgat	gtggagggtgc	acacagctca	gacgcaaccc	900
cgggaggagc	agttcaaacag	cacttccgc	tcagtcagtg	aacttcccat	catgcaccag	960
gactggctca	atggcaagga	gttcaaatgc	agggtaaca	gtgcagctt	ccctgcccc	1020
atcgagaaaa	ccatctccaa	accCAAAGGC	agaccgaagg	ctccacaggt	gtacaccatt	1080
ccacctccca	aggagcagat	gcccaaggat	aaagtca	tgacctgc	gataacagac	1140
ttcttccctg	aagacattac	tgtggagtg	cagtggat	ggcagccagc	ggagaactac	1200
aagaacactc	agcccatcat	ggacacagat	ggcttta	tcgtctacag	caagctcaat	1260
gtcagaaga	gcaactggga	gcaaggaaat	acttcac	gctctgtt	acatgagggc	1320
ctgcacaacc	accatactga	gaagagcctc	tcccactctc	ctggtaat	a	1371

<210> 83  
<211> 15  
<212> DNA  
<213> Oryctolagus cuniculus

<400> 83  
agcgatggaa taagc 15

<210> 84  
<211> 48  
<212> DNA  
<213> Oryctolagus cuniculus

<400> 84  
atcattagta gtgggtgaa cacatactac gcgagctggg caaaaggc 48

<210> 85  
<211> 24  
<212> DNA  
<213> Oryctolagus cuniculus

<400> 85  
gttgggtg gtacttata catc 24

<210> 86  
<211> 239  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> A synthetic 95F04 light chain sequence

<400> 86  
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Trp  
1 5 10 15  
Leu Pro Gly Ala Thr Phe Ala Gln Ala Val Val Thr Gln Thr Thr Ser  
20 25 30  
Pro Val Ser Ala Pro Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ser  
35 40 45

Ser	Gln	Ser	Val	Tyr	Gly	Asn	Asn	Glu	Leu	Ser	Trp	Tyr	Gln	Gln	Lys
50						55					60				
Pro	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Gln	Ala	Ser	Ser	Leu	Ala
65					70					75				80	
Ser	Gly	Val	Pro	Ser	Arg	Phe	Lys	Gly	Ser	Gly	Ser	Gly	Thr	Gln	Phe
						85			90				95		
Thr	Leu	Thr	Ile	Ser	Asp	Leu	Glu	Cys	Asp	Asp	Ala	Ala	Thr	Tyr	Tyr
						100			105				110		
Cys	Leu	Gly	Glu	Tyr	Ser	Ile	Ser	Ala	Asp	Asn	His	Phe	Gly	Gly	Gly
						115			120				125		
Thr	Glu	Val	Val	Val	Lys	Arg	Thr	Pro	Val	Ala	Pro	Thr	Val	Leu	Leu
						130			135				140		
Phe	Pro	Pro	Ser	Ser	Ala	Glu	Leu	Ala	Thr	Gly	Thr	Ala	Thr	Ile	Val
145						150				155				160	
Cys	Val	Ala	Asn	Lys	Tyr	Phe	Pro	Asp	Gly	Thr	Val	Thr	Trp	Lys	Val
						165			170				175		
Asp	Gly	Ile	Thr	Gln	Ser	Ser	Gly	Ile	Asn	Asn	Ser	Arg	Thr	Pro	Gln
						180			185				190		
Asn	Ser	Ala	Asp	Cys	Thr	Tyr	Asn	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser
						195			200				205		
Ser	Asp	Glu	Tyr	Asn	Ser	His	Asp	Glu	Tyr	Thr	Cys	Gln	Val	Ala	Gln
						210			215				220		
Asp	Ser	Gly	Ser	Pro	Val	Val	Gln	Ser	Phe	Ser	Arg	Lys	Ser	Cys	
						225			230				235		

<210> 87  
<211> 13  
<212> PRT  
<213> Oryctolagus cuniculus

<400> 87  
Gln Ser Ser Gln Ser Val Tyr Gly Asn Asn Glu Leu Ser  
1 5 10

<210> 88  
<211> 7  
<212> PRT  
<213> Oryctolagus cuniculus

<400> 88  
Gln Ala Ser Ser Leu Ala Ser  
1 5

<210> 89  
<211> 11  
<212> PRT  
<213> Oryctolagus cuniculus

<400> 89  
Leu Gly Glu Tyr Ser Ile Ser Ala Asp Asn His  
1 5 10

<210> 90  
<211> 720  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> A synthetic 95F04 anti-CD83 light chain sequence

<400> 90	
atggacacga gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc	60
acatttgcac aaggcggtt gaccagact acatcgcccg tgcgtgcacc tggtggaggc	120
acagtcacca tcaattgcca gtccagtcag agtgtttatg gtaacaacga attatcctgg	180
tatcagcaga aaccaggcga gcctcccaag ctccgtatct accaggcatc cagcctggca	240
tctggggtcc catcgcggtt caaaggcagt ggatctggga cacagttcac tctcaccatc	300
agcgacactgg agtgtgacga tgctgccact tactactgtc taggcgaata tagcattagt	360
gctgataatc atttcggcgg agggaccgag gtgggtgtca aacgtacgccc agttgcacct	420
actgtcctcc tcttcccacc atctagcgt gagctggaa ctggaacacgc caccatcgtg	480
tgcgtggcga ataaatactt tcccgtatgac accgtcacct ggaagggtgga tggcatcacc	540
caaaggcagcg gcatcaataa cagtagaaaca ccgcagaatt ctgcagatt tacctacaac	600
ctcagcagta ctctgacact gaggcagcgcac gagtacaaca gccacgcacga gtacacctgc	660
caggtggccc aggactcagg ctcaccggc gtccagagct tcagtaggaa gagctgttag	720

<210> 91

<211> 460

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic 95F04 heavy chain sequence

<400> 91

Met	Glu	Thr	Gly	Leu	Arg	Trp	Leu	Leu	Leu	Val	Ala	Val	Leu	Lys	Gly
1				5				10					15		
Val	Gln	Cys	Gln	Ser	Val	Glu	Glu	Ser	Gly	Gly	Arg	Leu	Val	Thr	Pro
					20			25				30			
Gly	Thr	Pro	Leu	Thr	Leu	Thr	Cys	Thr	Val	Ser	Gly	Ile	Asp	Leu	Ser
					35			40				45			
Ser	Asn	Ala	Met	Ile	Trp	Val	Arg	Gln	Ala	Pro	Arg	Glu	Gly	Leu	Glu
					50			55			60				
Trp	Ile	Gly	Ala	Met	Asp	Ser	Asn	Ser	Arg	Thr	Tyr	Tyr	Ala	Thr	Trp
					65			70			75		80		
Ala	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Thr	Ser	Ser	Ile	Thr	Val	Asp
					85			90				95			
Leu	Lys	Ile	Thr	Ser	Pro	Thr	Thr	Glu	Asp	Thr	Ala	Thr	Tyr	Phe	Cys
					100			105				110			
Ala	Arg	Gly	Asp	Gly	Gly	Ser	Ser	Asp	Tyr	Thr	Glu	Met	Trp	Gly	Pro
					115			120				125			
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val
					130			135			140				
Tyr	Pro	Leu	Ala	Pro	Gly	Ser	Ala	Ala	Gln	Thr	Asn	Ser	Met	Val	Thr
					145			150			155		160		
Leu	Gly	Cys	Leu	Val	Lys	Gly	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Thr
					165			170			175				
Trp	Asn	Ser	Gly	Ser	Leu	Ser	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
					180			185			190				
Leu	Gln	Ser	Asp	Leu	Tyr	Thr	Leu	Ser	Ser	Ser	Val	Thr	Val	Pro	Ser
					195			200			205				
Ser	Thr	Trp	Pro	Ser	Glu	Thr	Val	Thr	Cys	Asn	Val	Ala	His	Pro	Ala
					210			215			220				
Ser	Ser	Thr	Lys	Val	Asp	Lys	Lys	Ile	Val	Pro	Arg	Asp	Cys	Gly	Cys
					225			230			235		240		
Lys	Pro	Cys	Ile	Cys	Thr	Val	Pro	Glu	Val	Ser	Ser	Val	Phe	Ile	Phe
					245			250			255				
Pro	Pro	Lys	Pro	Lys	Asp	Val	Leu	Thr	Ile	Thr	Leu	Thr	Pro	Lys	Val
					260			265			270				
Thr	Cys	Val	Val	Val	Asp	Ile	Ser	Lys	Asp	Asp	Pro	Glu	Val	Gln	Phe
					275			280			285				
Ser	Trp	Phe	Val	Asp	Asp	Val	Glu	Val	His	Thr	Ala	Gln	Thr	Gln	Pro
					290			295			300				

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro  
 305                   310                   315                   320  
 Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val  
 325                   330                   335  
 Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr  
 340                   345                   350  
 Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys  
 355                   360                   365  
 Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp  
 370                   375                   380  
 Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro  
 385                   390                   395                   400  
 Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser  
 405                   410                   415  
 Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala  
 420                   425                   430  
 Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His  
 435                   440                   445  
 His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys  
 450                   455                   460

<210> 92  
 <211> 5  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 92  
 Ser Asn Ala Met Ile  
 1                   5

<210> 93  
 <211> 16  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 93  
 Ala Met Asp Ser Asn Ser Arg Thr Tyr Tyr Ala Thr Trp Ala Lys Gly  
 1                   5                   10                   15

<210> 94  
 <211> 11  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 94  
 Gly Asp Gly Gly Ser Ser Asp Tyr Thr Glu Met  
 1                   5                   10

<210> 95  
 <211> 1383  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A synthetic 95F04 anti-CD83 heavy chain sequence

<400> 95  
 atggagactg ggctgcgctg gtttccctg gtcgtgtgc tcaaagggtgt ccagtgtcag       60  
 tcggtgagg agtccggggg tcgcctggc acgcctggg accccctgac actcacctgc       120  
 acagtctctg gaatcgacct cagtagcaat gcaatgatct gggtccgcca ggctccaagg       180  
 gaggggctgg aatggatcgg agccatggat agtaatagta ggacgtacta cgcgacctgg       240  
 gcgaaaggcc gattcaccat ctccagaacc tcgtcgatta cggtgatct gaaaatcacc       300

agtccgacaa	ccgaggacac	ggcccacatat	ttctgtgcca	gagggatgg	tggcagtagt	360
gattatacag	agatgtgggg	cccaggacc	ctcgaccc	tctcgagcgc	ttctacaaag	420
ggcccatctg	tctatccact	ggccccctgga	tctgtgccc	aaactaactc	catggtgacc	480
ctggatgccc	tggtaagggt	ctatccctt	gagccagtga	cagtgaccc	gaactcttgg	540
tccctgtcca	gcgggtgtca	cacccccc	gctgtcctgc	agtctgaccc	ctacactctg	600
agcagtcag	tgactgtccc	ctccagcacc	tggcccagcg	agaccgtcac	ctgcaacgtt	660
gcccacccgg	ccagcagcac	caaggtggac	aagaaaattt	tgcccaggg	ttgtgggtgt	720
aaggcttgc	tatgtacagt	cccagaagta	tcatctgtct	tcatcttccc	cccaaagccc	780
aaggatgtgc	tcaccattac	tctgactctt	aaggtcacgt	gtgttgtgtt	agacatcagc	840
aaggatgatc	ccgaggtcca	gttcagctgg	ttttagatg	atgtggaggt	gcacacagct	900
cagacgcaac	cccggggagga	gcagttcaac	agcactttcc	gctcagtcag	tgaacttccc	960
atcatgcacc	aggactggct	caatggcaag	gagttcaaat	gcaggggtcaa	cagtgcagct	1020
ttccctgccc	ccatcgagaa	aaccatctcc	aaaacccaaag	gcagaccgaa	ggctccacag	1080
gtgtacacca	ttccacactcc	caaggagcag	atggccaaagg	ataaaagtca	tctgacctgc	1140
atgataacag	acttcttccc	tgaagacatt	actgtggagt	ggcagtgaa	tggcagcca	1200
gcccggaaact	acaagaacac	ttagccatc	atggacacag	atggcttta	cttcgtctac	1260
agcaagctca	atgtgcagaa	gagcaactgg	gaggcaggaa	atactttcac	ctgctctgt	1320
ttacatgagg	gcctgcacaa	ccaccatact	gagaagagcc	tctcccactc	tcctggtaaa	1380
	tga					1383

<210> 96

<211> 1383

<212> DNA

<213> Artificial Sequence

<220>

<223> A synthetic 95F04 anti-CD83 light chain sequence

<400> 96

atggagactg	ggctgcgctg	gcttctcctg	gtcgctgtgc	tcaaagggtgt	ccagtgtcag	60
tccgtggagg	agtccccgggg	tccctggc	acgcctggg	caccctgtac	actcacctgc	120
acagtctctg	gaatcgacct	cagtagcaat	gcaatgatct	gggtccggca	ggctccaagg	180
gaggggctgg	aatggatcgg	agccatggat	agtaatagta	ggacgtacta	cgcgacctgg	240
gcgaaaggcc	gattcaccat	ctccagaacc	tcgtcgat	cggtggatct	gaaaatcacc	300
atccgcacaa	ccgaggacac	ggccacat	ttctgtgcca	gaggggatgg	tggcagtagt	360
gattatacag	agatgtgggg	cccaggacc	ctcgaccc	tctcgagcgc	ttctacaaag	420
ggcccatctg	tctatccact	ggccccctgga	tctgtgccc	aaactaactc	catggtgacc	480
ctggatgccc	tggtaagggt	ctatccctt	gagccagtga	cagtgaccc	gaactcttgg	540
tccctgtcca	gcgggtgtca	cacccccc	gctgtcctgc	agtctgaccc	ctacactctg	600
agacgtcag	tgactgtccc	ctccagcacc	tggcccgcc	agaccgtcac	ctgcaacgtt	660
gcccacccgg	ccagcagcac	caaggtggac	aagaaaattt	tgcccaggg	ttgtgggtgt	720
aaggcttgc	tatgtacagt	cccagaagta	tcatctgtct	tcatcttccc	cccaaagccc	780
aaggatgtgc	tcaccattac	tctgactctt	aaggtcacgt	gtgttgtgtt	agacatcagc	840
aaggatgatc	ccgagggtcca	gttcagctgg	ttttagatg	atgtggaggt	gcacacagct	900
cagacgcaac	cccggggagga	gcagttcaac	agcactttcc	gctcagtcag	tgaacttccc	960
atcatgcacc	aggactggct	caatggcaag	gagttcaaat	gcaggggtcaa	cagtgcagct	1020
ttccctgccc	ccatcgagaa	aaccatctcc	aaaacccaaag	gcagaccgaa	ggctccacag	1080
gtgtacacca	ttccacactcc	caaggagcag	atggccaaagg	ataaaagtca	tctgacctgc	1140
atgataacag	acttcttccc	tgaagacatt	actgtggagt	ggcagtgaa	tggcagcca	1200
gcccggaaact	acaagaacac	ttagccatc	atggacacag	atggcttta	cttcgtctac	1260
agcaagctca	atgtgcagaa	gagcaactgg	gaggcaggaa	atactttcac	ctgctctgt	1320
ttacatgagg	gcctgcacaa	ccaccatact	gagaagagcc	tctcccactc	tcctggtaaa	1380
	tga					1383

<210> 97

<211> 107

<212> PRT

<213> Homo sapiens

<400> 97

Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr

1

5

10

15

Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu  
     20                       25                       30  
 Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu  
     35                       40                       45  
 Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala  
     50                       55                       60  
 Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys  
   65                       70                       75                       80  
 Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg  
     85                       90                       95  
 Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr  
     100                       105

<210> 98  
 <211> 8  
 <212> PRT  
 <213> Oryctolagus cuniculus

<400> 98  
 Gln Ser Val Tyr Asp Asn Asp Glu  
   1                       5

<210> 99  
 <211> 720  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> A synthetic 96G08 anti-CD83 light chain sequence

<400> 99  
 atggacacga gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc     60  
 acatttgcgc aagtgtgac ccagactgca tcgcccgtgt ctgcacctgt gggaggcaca     120  
 gtcaccatca attgcaggc cagttagt gtttataata acgacttctt atcctggtat     180  
 cagcagaaac cagggcagcc tcccaaactc ctgatctatt atgcatccac tctggcatct     240  
 ggggtccat ccccggtcaa aggcatgtga tctggacac agttcactct caccatcagc     300  
 gacctggagt gtgacgatgc gccacttact actgtacagg cacttatggt aatagtgttt     360  
 ggtacgagga tgcttcggc ggagggaccc aggtgggtggt caaacgtacg ccagttgcac     420  
 ctactgtcct cctttccca ccatctagcg ctgagctggc aactggaaaca gccaccatcg     480  
 tttgcgtggc gaataaatac ttccccatgc gcaccgtcac ctgaaagggtg gatggcatca     540  
 cccaaagcag cggcatcaat aacagttagaa caccgcagaa ttctgcagat tgtacctaca     600  
 acctcagcag tactctgaca ctgagcagcg acgagttacaa cagccacgac gagtacacct     660  
 gccaggtggc ccaggactca ggctcacccgg tcgtccagag cttcagtagg aagagctgtt     720